



SEQUENCE LISTING

<110> Bunney Jr., William E.
Jones, Edward G.
Molnar, Margherita
The Board of Trustees of The Leland Stanford
Junior University

<120> Genes Involved in Neuropsychiatric Disorders

<130> 020885-000720US

<140> US 10/649,400

<141> 2003-08-26

<150> US 60/406,879

<151> 2002-08-28

<150> US 60/451,306

<151> 2003-02-27

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<170> PatentIn Ver. 2.1

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<212> DNA

<213> Homo sapiens

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alpha-B subunit (CAMKII-alpha) cDNA

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<222> (7)..(1476)

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<222> (874)..(1223)

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<212> PRT

<213> Homo sapiens

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alpha-B subunit (CAMKII-alpha)

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Val Leu Ala Gly Gln Glu Tyr Ala Ala Lys Ile Ile Asn Thr Lys Lys
      35                      40                     45

Leu Ser Ala Arg Asp His Gln Lys Leu Glu Arg Glu Ala Arg Ile Cys
      50                      55                     60

Arg Leu Leu Lys His Pro Asn Ile Val Arg Leu His Asp Ser Ile Ser
      65                      70                     75                     80

Glu Glu Gly His His Tyr Leu Ile Phe Asp Leu Val Thr Gly Gly Glu
      85                      90                     95

Leu Phe Glu Asp Ile Val Ala Arg Glu Tyr Tyr Ser Glu Ala Asp Ala
      100                     105                     110

Ser His Cys Ile Gln Gln Ile Leu Glu Ala Val Leu His Cys His Gln
      115                     120                     125

Met Gly Val Val His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu Ala
      130                     135                     140

Ser Lys Leu Lys Gly Ala Ala Val Lys Leu Ala Asp Phe Gly Leu Ala
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Ile Glu Val Glu Gly Glu Gln Gln Ala Trp Phe Gly Phe Ala Gly Thr
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Pro Gly Tyr Leu Ser Pro Glu Val Leu Arg Lys Asp Pro Tyr Gly Lys
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<213> Homo sapiens

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<223> T-brain-1 (TBR1)

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Val Leu His Asp His Pro Ile Ile Ser Thr Thr Asp Asn Leu Glu Arg
          35                      40                      45

Ser Ser Pro Leu Lys Lys Ile Thr Arg Gly Met Thr Asn Gln Ser Asp
          50                      55                      60

Thr Asp Asn Phe Pro Asp Ser Lys Asp Ser Pro Gly Asp Val Gln Arg
          65                      70                      75                      80

Ser Lys Leu Ser Pro Val Leu Asp Gly Val Ser Glu Leu Arg His Ser
          85                      90                      95

Phe Asp Gly Ser Ala Ala Asp Arg Tyr Leu Leu Ser Gln Ser Ser Gln
          100                      105                      110

Pro Gln Ser Ala Ala Thr Ala Pro Ser Ala Met Phe Pro Tyr Pro Gly
          115                      120                      125

Gln His Gly Pro Ala His Pro Ala Phe Ser Ile Gly Ser Pro Ser Arg
          130                      135                      140

Tyr Met Ala His His Pro Val Ile Thr Asn Gly Ala Tyr Asn Ser Leu
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Leu Ser Asn Ser Ser Pro Gln Gly Tyr Pro Thr Ala Gly Tyr Pro Tyr
          165                      170                      175

Pro Gln Gln Tyr Gly His Ser Tyr Gln Gly Ala Pro Phe Tyr Gln Phe
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Ser Ser Thr Gln Pro Gly Leu Val Pro Gly Lys Ala Gln Val Tyr Leu
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Cys Asn Arg Pro Leu Trp Leu Lys Phe His Arg His Gln Thr Glu Met
          210                      215                      220

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Pro	Gln	Arg	Trp	Phe	Val	Thr	Pro	Ala	Asn	Asn	Arg	Leu	Asp	Phe	Ala	485	490		495
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Leu	Leu	Ser	Tyr	Ala	Ala	Ala	Gly	Val	Lys	Ala	Leu	Pro	Leu	Gln	Ala	515	520		525
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 Arg Ser Pro Leu Pro Pro Gly Ala Ala Glu Asp Ala Lys Pro Lys Asp
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Glu Val Ile Leu Ala Glu Asp Lys Arg Thr Gln Lys Leu Val Ala Ile
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Lys Cys Ile Ala Lys Glu Ala Leu Glu Gly Lys Glu Gly Ser Met Glu
      50             55             60

Asn Glu Ile Ala Val Leu His Lys Ile Lys His Pro Asn Ile Val Ala
      65             70             75             80

Leu Asp Asp Ile Tyr Glu Ser Gly Gly His Leu Tyr Leu Ile Met Gln
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Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Val Glu Lys Gly Phe
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Tyr Thr Glu Arg Asp Ala Ser Arg Leu Ile Phe Gln Val Leu Asp Ala
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Val Lys Tyr Leu His Asp Leu Gly Ile Val His Arg Asp Leu Lys Pro
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Glu Asn Leu Leu Tyr Tyr Ser Leu Asp Glu Asp Ser Lys Ile Met Ile
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Ser Asp Phe Gly Leu Ser Lys Met Glu Asp Pro Gly Ser Val Leu Ser
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Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val Leu Ala Gln
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Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly Val Ile Ala
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Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Asp Glu Asn Asp Ala
      210            215            220

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 His Pro Trp Ile Ala Gly Asp Thr Ala Leu Asp Lys Asn Ile His Gln
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 Leu Gly Thr Ser Gln Glu Gly Gln Gly Gln Thr Ala Ser His Gly Glu
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<210> 7
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 <213> Artificial Sequence

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 flexible linker

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 <222> (6)..(200)
 <223> Gly residues from position 6 to 200 may be present
 or absent

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 65 70 75 80

10